



Blast 2 Sequences results

(iv)

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

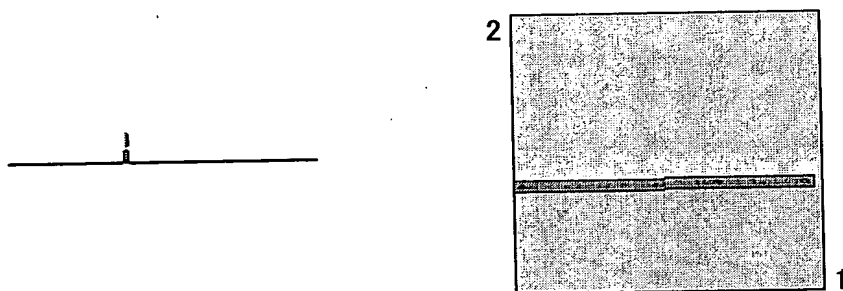
Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ View option
 Masking character option Masking color option
☐ Show CDS translation

Sequence 1: lcl|1_seq_1

Length = 31 (1 .. 31)

Sequence 2: lcl|2_seq_2

Length = 4258 (1 .. 4258)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 60.3 bits (31), Expect = 1e-07
 Identities = 31/31 (100%), Gaps = 0/31 (0%)
 Strand=Plus/Plus

```
Query 1      AAGCCGACTTCCAGATCTACTCGGAGTACTG 31
            |||
Sbjct 1626   AAGCCGACTTCCAGATCTACTCGGAGTACTG 1656
```

CPU time: 0.01 user secs. 0.00 sys. secs 0.01 total secs.

Lambda K H
 1.33 0.621 1.12

Gapped
 Lambda K H
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Sequences: 1

BEST AVAILABLE COPY

Blast Result

Number of Hits to DB: 7
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 31
Length of database: 18,725,440,322
Length adjustment: 22
Effective length of query: 9
Effective length of database: 18,725,440,300
Effective search space: 168528962700
Effective search space used: 168528962700
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 18 (35.3 bits)

BEST AVAILABLE COPY